PFRP

Pelagic Fisheries Research Program

Volume 1, Number 1

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Pelagic Fisheries Research Program

Pelagic fisheries in the western Pacific Ocean have tremendous economic importance. According to the Forum Fisheries Agency, the tuna harvested in the waters within and adjacent to the Exclusive Economic Zone (EEZ) of the U.S. islands in the Pacific in 1995 had an estimated value of US$1.7 billion, and the pelagic fish in the EEZ of U.S. islands in the Pacific is valued at approximately US$400 million.

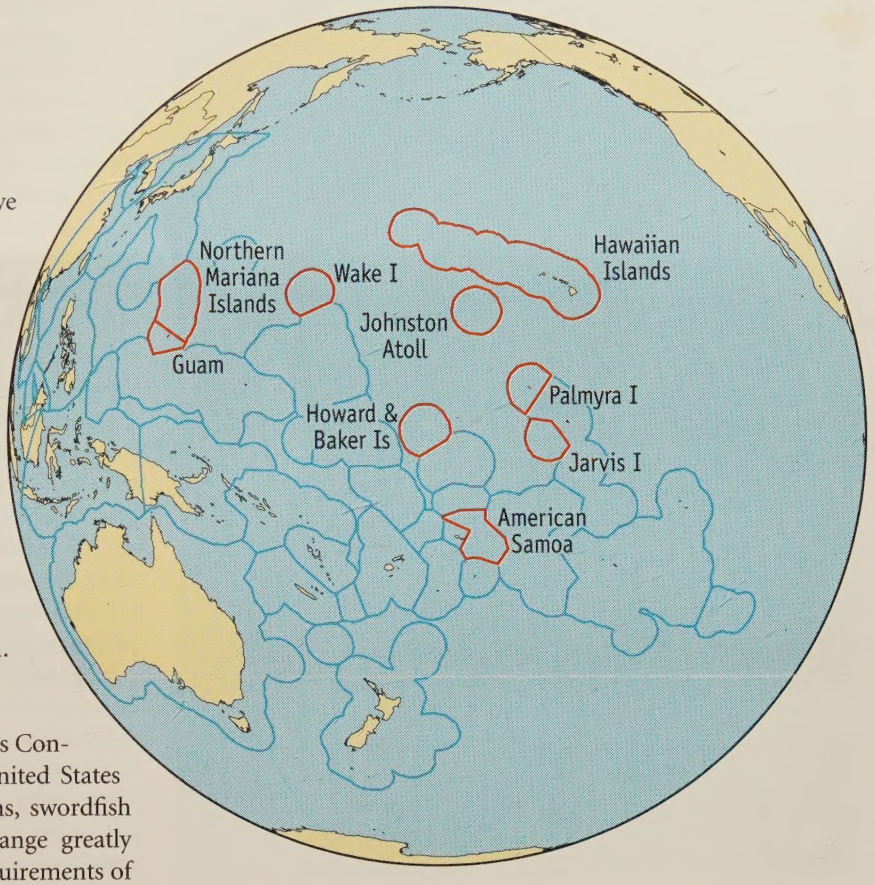

Figure 1. Exclusive economic zones (EEZs) of Pacific Islands. Western Pacific Regional Fisheries Management Council jurisdiction shown in red.

In 1992, an amendment to the Magnuson Fisheries Conservation and Management Act of 1976 gave the United States legal mandate to regulate fisheries for tunas, marlins, swordfish and other "highly migratory" pelagic fish. The change greatly increased the responsibilities and the information requirements of the Western Pacific Regional Fishery Management Council (WPRFMC), which is responsible for fisheries management of the EEZ (from three to 200 nautical miles offshore) of U.S. islands in the Pacific. These islands include American Samoa, Guam, Hawai'i, the Northern Mariana Islands, Wake Island, Johnston Atoll, Palmyra and Jarvis Islands, and Howard and Baker Islands (Figure 1).

To supplement scientific information available to the WPRFMC, the Pelagic Fisheries Research Program (PFRP) was created and placed in the Joint Institute for Marine and Atmospheric Research (JIMAR) at the University of Hawai'i at Mānoa, School of Ocean and Earth Science and Technology (SOEST). JIMAR is one of several National Oceanic and Atmospheric Administration (NOAA) Joint Institutes set up to foster collaboration between NOAA and university scientists. JIMAR was selected as the site for the PFRP because of its distinguished record of productive collaboration between University of Hawai'i and National Marine Fisheries Service (NMFS) scientists since 1977.

The Magnuson Act stipulates that the goal of the fisheries management is "optimal use." This goal requires that, in addition to the traditional biological and ecological factors, social and economic factors must also be considered. Consequently, the range of subjects studied by PFRP projects is very wide and includes biology, statistics, economics and sociology.

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PFRP Achievements

- A reliable data base on pelagic fishing in Hawaii that extends to the 1950s has been compiled, making it possible to evaluate potential effects of increased fishing pressure on tuna populations in the Hawaii EEZ.
- The economic performance of the Honolulu-based longline fleet has been thoroughly analyzed. This information has already been used to evaluate the possible economic impacts of imposing new regulations on the longline fleet.
- A thorough study of the surface currents around the Hawaii archipelago using satellite-tracked drifting buoys and computer modeling has been completed. The results show a unique circulation system that has important implications for juvenile tuna, including their survivability and ultimate availability to fisheries. These results could also be applied to search-and-rescue and pollution-control operations.
- Studies of the large-scale movement of skipjack and yellowfin tunas, using tagging data in collaboration with scientists from the South Pacific Commission and Japan have been completed. These results can be used to determine the effects of large-scale fisheries near the equator on fisheries in other areas.

Since 1993, the PFRP has funded 35 different projects, which range from the distinctly unglamorous, e.g., sifting through data archives for reliable information, to the state of the art "high tech," such as the use of DNA to identify races of blue marlin and swordfish. Many of these projects are in their final phases, and 1996 is the first year during which nearly as many projects were completed as new projects were initiated.

This inaugural issue of the PFRP Newsletter features the results of the research into stock structure of blue marlin and swordfish and describes ongoing research into the genetics of dolphinfish (i.e., mahimahi) and bigeye tuna. Future issues will describe results of other projects. For a description of all projects, consult the PFRP World Wide Web site at http://www/soest.hawaii.edu/rbailey/prf1.html.

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Using DNA to Analyze the Population Structure of Swordfish and Pacific Blue Marlin

- *A 1,635-pound marlin landed in recent years had the potential of becoming a world-record black marlin until a genetic analysis by PFRP scientists identified the billfish as a blue marlin.*
- *Genetic analysis of fish tissue by the scientists has also led to an arrest at a Virginia fish market where Atlantic sailfish was being sold as "striped marlin from Ecuador."*
- *But the main purpose of the PFRP-funded research project headed by Principal Investigators John E. Graves of the Virginia Institute of Marine Science, College of William and Mary, and Barbara A. Block, Hopkins Marine Station, Stanford University, is to identify the population structure of broadbill swordfish (*Xiphias gladius*) and blue marlin (*Makaira nigricans*) for fishery management purposes.*

According to tag-and-release studies, marlin and swordfish are capable of large-scale movements that cover thousands of kilometers. For example, a swordfish tagged northeast of the Hawaiian Islands was recaptured off the coast of California, a straight-line distance of approximately 3000 km. But do such long-distance recaptures mean that all swordfish belong to a single, worldwide stock or to particular basinwide stocks, e.g., Pacific, Atlantic and Mediterranean? And if the species is distributed into more than one stock, what are the distribution limits of each stock? And what is the amount, if any, of genetic-mixing between the stocks?

Answering questions such as these is essential if effective fishery management policies are to be developed. If the populations of a fishery are highly structured, that is, there is little mixing of the populations, then management directives aimed at a broad geographic area would be inappropriate and could lead to the irrevocable loss of regional populations, decreasing the genetic diversity and evolutionary potential of the species. On the other hand, management efforts divided on too fine a scale may be overly restrictive.

Applying Biotechnology to Billfishes

Genetic techniques have proven to be powerful tools for examining questions of population structure and migratory movements in terrestrial and marine species. For example, they have been used to obtain population structure and mating systems for minke whales and to resolve genetic relationships between closely related human populations. Two pieces of genetic material well suited for looking at differences that might occur within a species are mitochondrial DNA (mtDNA) and microsatellite DNA.

MtDNA is extracted from an organism's mitochondria—small structures found in all cells. When used to examine billfish, the mtDNA is purified from heart, skeletal muscle or liver tissue of the fish. The mtDNA is then subjected to chemical processes that cut the mtDNA molecules at specific places. Sequences of genes in

these mtDNA parts indicate genetic differences. In other words, the mtDNA sequences provide a "genetic fingerprint" for each individual fish.

Microsatellite DNA is similar to mtDNA, but is found in the cell nucleus and evolves at a much faster rate. Sequencing the short and highly variable microsatellite DNA can be used to detect even higher levels of genetic difference than is possible through sequencing mtDNA. Another advantage to microsatellite DNA is its inheritance from both parents. MtDNA, on the other hand, is inherited from the mother only.

Once genetic material is analyzed, patterns of distribution are considered. If the distribution of genetic types is different among samples from different areas, then one can infer that very little mixing of stocks is occurring. On the other hand, if the distribution of the genetic types is similar between locations, one can assume that enough mixing is occurring to prevent the accumulation of genetic differences.

Blue Marlin

Since 1990, John Graves and Jan McDowell have been investigating the global population structure of blue marlin. To assess the significance of differences in genetic distributions between collections of blue marlin from different geographic areas, they needed to determine if the distribution at a single location was stable over time. Therefore, they analyzed blue marlin collected at the Hawaiian International Billfish Tournament (HIBT) over several years. The results suggested that over time there is stability to genetic distributions. In other words, they were collecting from the same genetic stock of fish each year.

But were the Hawaiian blue marlin genetically similar to those collected in other regions of the Pacific Ocean? To address this question, Graves and McDowell compared their HIBT sample of blue marlin with samples from Ecuador, Mexico and Australia. The samples did not show significant genetic differences within the Pacific Ocean, which suggests at least a minimal amount of exchange and mating between fish from different areas. These findings are consistent with the long-distance recoveries of tagged fish.

On a global scale, the genetic studies indicate that blue marlin from the Pacific and Atlantic Oceans are not different species. In fact, several mtDNA types are common to fish from both oceans. However, there are major differences in the distribution of mtDNA types between samples of fish from the two oceans. All Pacific blue marlin and slightly more than half of Atlantic blue marlin share a group of closely related mtDNA types, which are referred to as ubiquitous. However, about 45 percent of Atlantic blue marlin have mtDNA types that differ from the ubiquitous types by several consistent differences (Figure 2). This same pattern of mtDNA type distribution and relationships is also evident in Pacific and Atlantic sailfish (*Istiophorus platypterus*).

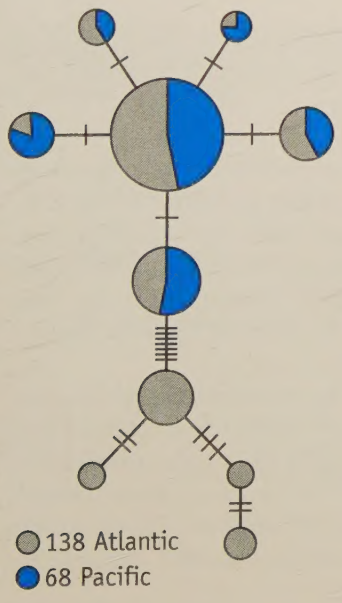

Figure 2. Blue Marlin mtDNA Types (n>2). The area of each circle is proportional to the number of individuals with that mtDNA type. A "ubiquitous" group of mtDNA types is found in all Pacific blue marlin and just more than half of Atlantic blue marlin. The remaining Atlantic blue marlin have mtDNA types that as a group are closely related but quite distinct from those of the "ubiquitous" group.

These results provide insight into the evolutionary history of blue marlin and suggest a time of considerable isolation between the "ubiquitous" and "Atlantic" groups of blue marlin. Graves and McDowell suggest this isolation period could have occurred during a cold period when gene flow around the Cape of Good Hope was not possible for tropical marine organisms, with subsequent movement (and proliferation) of blue marlin from the Pacific to the Atlantic when waters warmed.

These results also provide a way to positively identify about one-half of all Atlantic blue marlin and offer a strong basis for enforcing the U.S. Fishery Management Plan that allows the sale of Pacific blue marlin but not Atlantic blue marlin.

Swordfish

At Hopkins Marine Station, Stanford University, Patricia Rosel and Barbara Block have been using mtDNA to analyze swordfish samples from the Pacific, Atlantic and Mediterranean. Their results suggest that swordfish, like blue marlin and sailfish, fall into two distinct groups, i.e., a larger group containing genetic types from all sampling locations worldwide and a second, smaller group comprising only Atlantic and Mediterranean samples.

Rosel and Block propose that the reason for the existence of the two swordfish groups could be fidelity to spawning grounds by Mediterranean swordfish. They note that the estimated 14°C sea surface temperatures for the Cape of Good Hope during the height of the last glacial period (18,000 years ago) may have been low enough to inhibit the migration of blue marlin and sailfish but may not have been low enough to halt the migration of swordfish. Acoustic telemetry data indicate swordfish regularly make excursions into water as cold as 6°C. Nevertheless, Rosel and Block do not rule out the possibility that the water temperatures could have been sufficiently cold to pose a barrier to swordfish at some other time in the past.

Another outcome of Rosel and Block's comparison of mtDNA sequences of swordfish is the possibility of some degree of genetic cross-ocean basin isolation among Pacific swordfish. Pairwise comparison of West Pacific samples (Taiwan, Japan) versus the East Pacific samples (Mexico, Chile) were higher than pairwise comparisons of populations from the same side of the Pacific.

Due to the close genetic similarity between Pacific swordfish populations, research to determine possible basinwide subdivisions using mtDNA types would require increasing sample sizes to hundreds of individuals (which is logistically difficult). Therefore, in an ongoing PFRP-funded project, Block and postdoctoral associate Carol Reeb are analyzing genetic differences of swordfish samples using microsatellite DNA.

As part of their study, Block and Reeb plan to compare Chilean samples with Atlantic fish and western Pacific fish in order to investigate whether gene flow occurs around South America. Dispersal is generally thought to occur around southern Africa because waters there are warmer than southern America (Figure 3).

Block and Reeb also plan to investigate whether male and female swordfish share the same geographic partitioning and whether swordfish larvae show the same genetic composition and partitioning as adults. Such information could increase our awareness of swordfish behavior and the location of swordfish spawning grounds.

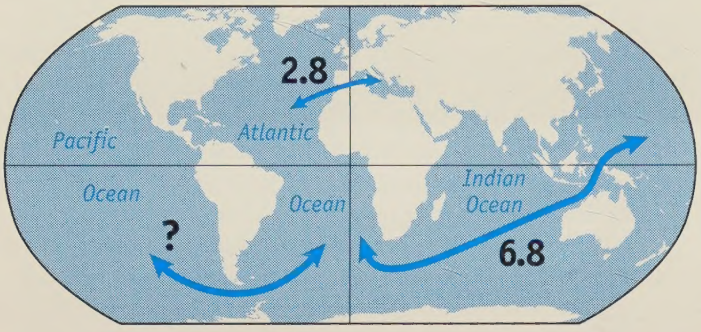

Figure 3. Gene Flow Between Ocean Basins. Number near arrow is the number of swordfish migrating each generation inferred from the analysis of mtDNA by Rosel and Block. Dispersal is generally thought to occur around southern Africa. However, a comparison of Chilean, Atlantic and Western Pacific samples may show that gene flow might be occurring around southern America.

Conclusion

A steady decrease in the mean size of swordfish catches in the Atlantic and Mediterranean Oceans, as well as significant declines in catch per unit effort in some areas, has led some nations to adopt measures to reduce fishing effort on Atlantic swordfish stocks. Similar decrease in Atlantic blue marlin has led to a U.S. Fishery Management Plan that bans the sale of Atlantic blue marlin. In the Pacific Ocean, particularly in the Hawaiian Islands, a recent influx of longline vessels in the U.S. domestic fishery, as well as an increase in the use of longline techniques common in the western North Atlantic, has resulted in a rapid increase in U.S. landing of Pacific billfish over the past five years.

To avoid possible irrevocable depletion of stocks and to maintain a viable commercial yield, it is necessary to manage billfish populations such that fishing pressure does not exceed a populations' ability to sustain it. Several recent scientific management panels have agreed that identification of billfish stock structure is a primary need.

Research into a species' population stock structure provides us with an understanding of the ranges and composition of fishery management units. The PFRP-funded studies headed by Graves and Block have established that a global population structure does exist for both blue marlin and swordfish. A further PFRP-funded study headed by Block aims to explore the possibility of a Pacific Ocean population structure for swordfish.

Bigeye Tuna Population Structure in the Pacific Ocean

In the western Pacific, several island countries are in the process of developing longline fleets, either locally owned or under joint venture arrangements, to target bigeye tuna for the Japanese sashimi market. With the distant-water fleets of Japan and Korea likely to maintain effort at recent levels, these locally based fleets in countries such as Fiji, Palau, the Federated States of Micronesia, the Marshall Islands, Papua New Guinea and Solomon Islands will see bigeye exploitation rates increase in coming years. Accurate stock assessment in support of fishery management will be in the long-term interests of all participants in the bigeye fishery.

The National Research Institute of Far Seas Fisheries in Japan, which has carried out most of the stock of assessment work on Pacific bigeye tuna (*Thunnus obesus*) to date, has concluded that the Pacific-wide bigeye stock has been in continuous decline since the late 1950s and that recent Pacific-wide catches have been in excess of the estimated maximum sustainable yield (MSY) of 120,000 t (Figure 4, page 6).

These interpretations—based on catch-per-unit-of-effort (CPUE) abundance indices and production-model estimates of MSY—assume that there is a single, Pacific-wide bigeye stock. The assumption, however, has never been tested despite information that questions such a hypothesis:

- Tagging data for bigeye have so far failed to demonstrate trans-Pacific movement.
- Larval distribution data suggest separate concentrations of bigeye larvae in the far western, central and eastern Pacific Ocean.
- There is a strong geographic trend in bigeye CPUE by longliners from the western (low CPUE) to the eastern Pacific.
- Yellowfin, a species with similar life history characteristics to bigeye, has been shown to comprise genetically distinct eastern and western Pacific stocks.

The uncertainty regarding bigeye stock structure in the Pacific is being addressed in an ongoing project, co-funded by the PFRP and the Forum Fisheries Agency, and conducted under the direction of Dr. John Hampton, principal fisheries scientist, South Pacific Commission, Noumea, New Caledonia, and Dr. Peter Grewe, research scientist, CSIRO Division of Fisheries, Hobart, Australia.

The objective of the research is to characterize the genetic variability within and among samples of bigeye tissue collected from seven locations across the tropical Pacific Ocean, including the Philippines, the Federated States of Micronesia, Kiribati, Hawai'i, Tahiti, and two Eastern Tropical Pacific locations. Genetic analysis involves the assessment of both mtDNA and DNA microsatellite

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The PFRP operates under the general direction of a Steering Committee, who meet periodically. Gathered at a recent meeting are (*from left*) Michael Laurs, director, NMFS Honolulu Laboratory; John Sibert, program manager, PFRP; Barry Raleigh, dean, SOEST; Kitty Simonds, executive director, WPRFMC; Gary Sakagawa, coordinator of Pelagics Research, NMFS Southwest Fishery Science Center; Mike Tillman, director, SW Fisheries Science Center, La Jolla; and Tom Schroeder, acting director, JIMAR. Sibert and Tillman attended the meeting as guests. Committee member Paul Callaghan, chairman, WPRFMC Scientific and Statistical Committee (*not pictured*), participated in the meeting via telephone from Guam.

Were Dolphinfish Once an Endangered Species?

Genetic analysis of several pelagic fish populations indicated a period of instability about 18,000 years ago during the Pleistocene period (characterized by the spreading and recession of continental ice sheets). Recent data analyzed at Hopkins Marine Station, Stanford University, by Carol Reeb, in a PFRP-funded project, indicate that dolphinfish, or mahimahi (*Coryphaena hippurus*), were no exception.

Using mtDNA to analyze the genetic composition of 55 dolphinfish from a collection of 200 samples collected from 11 sites worldwide, Reeb found 13 genetic types. One of these types was found to be very common and distributed worldwide while the remaining 12 were quite rare.

While the data to date has not been useful in discerning population subdivisions, it does suggest that dolphinfish had faced one of three scenarios: (1) a catastrophic near extinction, (2) demographic parameters favoring males, or (3) recurrent extinction and recolonization of populations.

As the research continues, Reeb is concentrating her efforts on locating a faster-evolving part of the mtDNA to better study population structure of the species. She has discovered that dolphinfish possess a very large mtDNA region that appears to be similar to a rapidly-evolving microsatellite sequence. Reeb has devised a novel and quick method to screen this molecular marker and hopes to use it to complete analysis of the 200 collected samples by the end of 1996.

Dolphinfish is an important component of local fisheries in many WPRFMC areas. However, to date, little is known about their stock structure, and no estimate of sustainable yield is available.

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Up-coming Events

October 21–24, 1996

Establishing a Sustainable Island-Based Tuna Industry
Maui Pacific Center, (808) 875-2310

November 4–6, 1996

Getting Ahead of the Curve: A Symposium on Managing Highly Migratory Fish of the Pacific Ocean
Monterey, California; National Coalition for Marine Conservation (703) 777-0037.

November 15, 1996

Meeting of PFRP Principal Investigators
Honolulu, Pelagic Fisheries Research Program
(808)956-4109.

Bigeye tuna population (continued from page 4)

variations, making the analyses more powerful and allowing for assessment of the relative effectiveness of these two genetic techniques.

The project will contribute to a better understanding of bigeye tuna stock structure in the Pacific Ocean, enabling scientists and fisheries managers to have better confidence in the regional bigeye assessment carried out to date. The project will also contribute to other PFRP projects concerned with the evaluation of catch-and-effort data for longline and other fisheries in the Hawai'i EEZ and surrounding areas by clarifying the linkages of bigeye in Hawaiian waters (where recent longline catches of the species have reached 1,500 t) with those of the western and eastern Pacific (with total Pacific-wide catches estimated at 120,000–160,000 t).

Grewe will present the project results at the *World Meeting on Bigeye Tunas* in La Jolla, California, November 12–16, 1996.

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Figure 4. Tuna being auctioned in Honolulu. With sashimi-quality tuna in high demand, the Pacific-wide catch of bigeye tuna has reached 152,000 t. A single ocean-wide bigeye stock is assumed, suggesting catches have exceeded maximum sustainable yield. The assumption, however, has never been tested. (photo courtesy of NMFS Honolulu Laboratory)

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